

520

RAW SEQUENCE LISTING

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Application Serial Number: 10/519,826
Source: PCT/10
Date Processed by STIC: 1/10/06

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DATE: 01/10/2006

PATENT APPLICATION: US/10/519,826

TIME: 11:49:55

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Output Set: N:\CRF4\01102006\J519826.raw

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3 <110> APPLICANT: Walther, Diego
4   Bader, Michael
6 <120> TITLE OF INVENTION: Neuronally Expressed Tryptophane Hydroxylase And its Use
8 <130> FILE REFERENCE: BB-123
10 <140> CURRENT APPLICATION NUMBER: 10/519,826
11 <141> CURRENT FILING DATE: 2004-12-30
13 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07744
14 <151> PRIOR FILING DATE: 2003-07-16
16 <150> PRIOR APPLICATION NUMBER: DE 10232151.5
17 <151> PRIOR FILING DATE: 2002-07-16
19 <160> NUMBER OF SEQ ID NOS: 14
21 <170> SOFTWARE: PatentIn version 3.3
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24 <211> LENGTH: 2350
25 <212> TYPE: DNA
26 <213> ORGANISM: homo sapiens
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33 aagaatatta caccgggata catgcagcca gcaatgatga tgttttccag taaatactgg      180
35 gcacggagag gggtttccct ggattcagca gtgcccgaag agcatcagct acttggcagc      240
37 tcaacactaa ataaacctaa ctctggcaaa aatgacgaca aaggcaacaa ggggaagcagc      300
39 aaacgtgaag ctgctaccga aagtggcaag acagcagttg ttttctcctt gaagaatgaa      360
41 gttggtggat tggtaaaagc actgaggctc tttcaggaaa aacgtgtcaa catgggtcat      420
43 attgaatcca ggaaatctcg gcgaagaagt tctgagggtg aaatctttgt ggactgtgag      480
45 tgtgggaaaa cagaattcaa tgagctcatt cagttgctga aatttcaaac cactattgtg      540
47 acgctgaatc ctccagagaa catttggaaca gaggaagaag agctagagga tgtgccctgg      600
49 ttccctcgga agatctctga gttagacaaa tgctctcaca gagttctcat gtatggttct      660
51 gagcttgatg ctgaccaccc aggatttaag gacaatgtct atcgacagag aagaaagtat      720
53 tttgtggatg tggccatggg ttataaatat ggtcagccca ttcccagggt ggagtatact      780
55 gaagaagaaa ctaaaacttg ggggtgttga ttccgggagc tctccaaact ctatcccact      840
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59 gaggacaatg tgcctcaact cgaagatgtc tccatgtttc tgaaagaaaag gtctggcttc      960
61 acggtgagggc cgggtggctgg atacctgagc ccacgagact ttctggcagg actggcctac     1020
63 agagtgttcc actgtaccca gtacatccgg catggctcag atccccctcta cccccagaa     1080
65 ccagacacat gccatgaact cttgggacat gttccactac ttgcggatcc taagtttgct     1140
67 cagttttcac aagaaatagg tctggcgtct ctgggagcat cagatgaaga tgttcagaaa     1200
69 ctagccacgt gctatttctt cacaatcgag tttggccttt gcaagcaaga agggcaactg     1260
71 cgggcatatg gagcaggact cctttcctcc attggagaat taaagcacgc cctttctgac     1320
73 aaggcatgtg tgaaagcctt tgaccctaaag acaacttgct tacaggaatg ccttatcacc     1380
75 accttccagg aagcctactt tgtttcagaa agttttgaag aagccaaaga aaagatgagg     1440
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85 ataacgcaaa taaccttctg tgtcatggct tggctaataa gcatgcaatt ccatatatct 1740
87 ataccatctt gtaactcact gtgttagtat ataaagcacc ataagaaatc caatggcaga 1800
89 taacctgaaa taacgtatta tgtttaaaca tcttaaaaag atttgacatt cctgcttagt 1860
91 gtccttaacc aaactgcac tagttaaaat ttgtaacaaa tagccctctt atgagtctca 1920
93 tttatgccct tttctttttc agatctaagc ctttctctctg tgttcattag ataaaatgaa 1980
95 aaaaagcagt gaagctgttt ccattttcaa tagtatcagt gttttcacgc attatttgag 2040
97 ataaacccag aattgtagga aacttcccat cacaataaca aaggttcaat attctatttc 2100
99 aaaaattggt gaggtaacac agcagttgga atgattttta ggttgagtat ttacacaatg 2160
101 caagaaaaca cttttttaca aatggaatta tgtaggttgc gttgaccttg tagaacctga 2220
103 gttatgacaa gcttcctgaa gtattttgga agatagtact tccggaagg acattaggaa 2280
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125 Ser Ser Thr Leu Asn Lys Pro Asn Ser Gly Lys Asn Asp Asp Lys Gly
126 35 40 45
129 Asn Lys Gly Ser Ser Lys Arg Glu Ala Ala Thr Glu Ser Gly Lys Thr
130 50 55 60
133 Ala Val Val Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Val Lys Ala
134 65 70 75 80
137 Leu Arg Leu Phe Gln Glu Lys Arg Val Asn Met Val His Ile Glu Ser
138 85 90 95
141 Arg Lys Ser Arg Arg Arg Ser Ser Glu Val Glu Ile Phe Val Asp Cys
142 100 105 110
145 Glu Cys Gly Lys Thr Glu Phe Asn Glu Leu Ile Gln Leu Leu Lys Phe
146 115 120 125
149 Gln Thr Thr Ile Val Thr Leu Asn Pro Pro Glu Asn Ile Trp Thr Glu
150 130 135 140
153 Glu Glu Glu Leu Glu Asp Val Pro Trp Phe Pro Arg Lys Ile Ser Glu
154 145 150 155 160
157 Leu Asp Lys Cys Ser His Arg Val Leu Met Tyr Gly Ser Glu Leu Asp
158 165 170 175
161 Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr Arg Gln Arg Arg Lys
162 180 185 190
165 Tyr Phe Val Asp Val Ala Met Gly Tyr Lys Tyr Gly Gln Pro Ile Pro
166 195 200 205
169 Arg Val Glu Tyr Thr Glu Glu Thr Lys Thr Trp Gly Val Val Phe
170 210 215 220
173 Arg Glu Leu Ser Lys Leu Tyr Pro Thr His Ala Cys Arg Glu Tyr Leu
174 225 230 235 240

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182           260           265           270
185 Phe Thr Val Arg Pro Val Ala Gly Tyr Leu Ser Pro Arg Asp Phe Leu
186           275           280           285
189 Ala Gly Leu Ala Tyr Arg Val Phe His Cys Thr Gln Tyr Ile Arg His
190           290           295           300
193 Gly Ser Asp Pro Leu Tyr Thr Pro Glu Pro Asp Thr Cys His Glu Leu
194 305           310           315           320
197 Leu Gly His Val Pro Leu Leu Ala Asp Pro Lys Phe Ala Gln Phe Ser
198           325           330           335
201 Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Asp Val Gln
202           340           345           350
205 Lys Leu Ala Thr Cys Tyr Phe Phe Thr Ile Glu Phe Gly Leu Cys Lys
206           355           360           365
209 Gln Glu Gly Gln Leu Arg Ala Tyr Gly Ala Gly Leu Leu Ser Ser Ile
210           370           375           380
213 Gly Glu Leu Lys His Ala Leu Ser Asp Lys Ala Cys Val Lys Ala Phe
214 385           390           395           400
217 Asp Pro Lys Thr Thr Cys Leu Gln Glu Cys Leu Ile Thr Thr Phe Gln
218           405           410           415
221 Glu Ala Tyr Phe Val Ser Glu Ser Phe Glu Glu Ala Lys Glu Lys Met
222           420           425           430
225 Arg Asp Phe Ala Lys Ser Ile Thr Arg Pro Phe Ser Val Tyr Phe Asn
226           435           440           445
229 Pro Tyr Thr Gln Ser Ile Glu Ile Leu Lys Asp Thr Arg Ser Ile Glu
230           450           455           460
233 Asn Val Val Gln Asp Leu Arg Ser Asp Leu Asn Thr Val Cys Asp Ala
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241 <210> SEQ ID NO: 3

242 <211> LENGTH: 2638

243 <212> TYPE: DNA

244 <213> ORGANISM: mus musculus

246 <400> SEQUENCE: 3

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251 tacatcgggg gccatgcagc ccgcaatgat gatgttttcc agtaaatact gggccaggag    180
253 agggttgtcc ttggattctg ctgtgccaga agatcatcag ctacttggca gcttaacaca    240
255 aaataaggct atcaaaagcg aggacaagaa aagcggcaaa gagcccggca aaggcgacac    300
257 cacagagagc agcaagacag cagttgtgtt ctccttgaag aatgaagttg gtgggctggt    360
259 gaaagcactt agactattcc aggaaaaaca tgtcaacatg cttcatatcg aatccaggcg    420
261 gtcccggcga agaagttctg aagtcgaaat cttcgtggac tgcaaatgtg gcaaaacgga    480
263 attcaatgag ctcattccagt tgctgaaatt tcagaccacc attgtgaccc tgaatccgcc    540
265 tgagagcatt tggacggagg aagaagatct cgaggatgtg ccgtggttcc ctcggaagat    600
267 ctctgagtta gacagatgct ctcaccagat cctcatgtac ggcaccgagc ttgatgccga    660
269 ccatccagga tttaaggaca atgtctatcg acagaggagg aagtattttg tggatgtggc    720

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275 gtacctgaaa aacctcccc tgctgaccaa gtactgtggc tacaggggaag acaacgtgcc      900
277 gcaactggaa gacgtctcca tgtttctgaa agagcgatct ggcttcacag tgagaccagt      960
279 ggctggctac ctgagcccaa gagacttcct ggcgggcttg gcctacagag tattccactg     1020
281 caccaggtac gtgcggcatg gctccgaccc cctctacacc ccggaaccag atacatgcca     1080
283 tgaactcttg ggacacgtgc cactgcttgc ggatcccaag tttgctcagt tttcccaaga     1140
285 gataggctta gcgtctctgg gagcctcaga tgaggacgtt cagaaactag ccacgtgcta     1200
287 tttcttcaca atcgagttcg gcctttgcaa gcaagagggt caactgcggg cgtatggagc     1260
289 agggttactt tcgtccatcg gagaattgaa gcatgctctt tccgacaagg cgtgtgtgaa     1320
291 atcctttgac ccaaagacga cctgcttgca ggaatgccta atcaccacct ttcaggacgc     1380
293 ttactttggt tcggacagtt ttgaagaagc caaagaaaag atgagggact ttgcaaagtc     1440
295 aattaccogt cccttctcgg tatacttcaa ccgctacacg cagagcattg aaattctgaa     1500
297 agacaccaga agtattgaga atgtggtgca ggacctgcgc agtgatttga acacagtgtg     1560
299 tgatgccttg aataaaaatga accaatatct ggggatttga tgcctagaac cagagttatt     1620
301 gtcagcatga gctcttgggg ggtgtagcaa caatgcagtc aatgttatcc aacatcaaca     1680
303 actttctgtg tcatggttgg ctagtaagca tgcaattctg tatgtccata cctctgtgta     1740
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313 aatgaaaat agttgggagg tggtttctat tttcaatagt atccgtgtta tttgagataa     2040
315 actagagttg ctccacgctt tgcatcacag caacaaagga tttaatattc tacttcagaa     2100
317 gctgttcaga aacacagcag ttgggatgga tgtagactga gtgttcagac aatgcaagca     2160
319 aagaaaagtt ttgataaaca ggatatatag gttgtactga cctcgttgaa accaatttgt     2220
321 ggcaagcttc ctgaagagct tctggaagga aacacttgaa caaagaatat tcgggaagct     2280
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325 cactgcaggc ttttgactcc ttttgcttag actgagaacc tcaaatcca cagggatgta     2400
327 aataccatct ctgattccaa agagttggag acggagtctg agagaaacaa agggatttgc     2460
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336 <210> SEQ ID NO: 4

337 <211> LENGTH: 488

338 <212> TYPE: PRT

339 <213> ORGANISM: mus musculus

341 <400> SEQUENCE: 4

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348          20          25          30
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352          35          40          45
355 Lys Glu Pro Gly Lys Gly Asp Thr Thr Glu Ser Ser Lys Thr Ala Val
356          50          55          60
359 Val Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Val Lys Ala Leu Arg
360 65          70          75          80
363 Leu Phe Gln Glu Lys His Val Asn Met Leu His Ile Glu Ser Arg Arg
364          85          90          95

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375 Thr Ile Val Thr Leu Asn Pro Pro Glu Ser Ile Trp Thr Glu Glu Glu
376      130      135      140
379 Asp Leu Glu Asp Val Pro Trp Phe Pro Arg Lys Ile Ser Glu Leu Asp
380 145      150      155      160
383 Arg Cys Ser His Arg Val Leu Met Tyr Gly Thr Glu Leu Asp Ala Asp
384      165      170      175
387 His Pro Gly Phe Lys Asp Asn Val Tyr Arg Gln Arg Arg Lys Tyr Phe
388      180      185      190
391 Val Asp Val Ala Met Gly Tyr Lys Tyr Gly Gln Pro Ile Pro Arg Val
392      195      200      205
395 Glu Tyr Thr Glu Glu Glu Thr Lys Thr Trp Gly Val Val Phe Arg Glu
396      210      215      220
399 Leu Ser Lys Leu Tyr Pro Thr His Ala Cys Arg Glu Tyr Leu Lys Asn
400 225      230      235      240
403 Leu Pro Leu Leu Thr Lys Tyr Cys Gly Tyr Arg Glu Asp Asn Val Pro
404      245      250      255
407 Gln Leu Glu Asp Val Ser Met Phe Leu Lys Glu Arg Ser Gly Phe Thr
408      260      265      270
411 Val Arg Pro Val Ala Gly Tyr Leu Ser Pro Arg Asp Phe Leu Ala Gly
412      275      280      285
415 Leu Ala Tyr Arg Val Phe His Cys Thr Gln Tyr Val Arg His Gly Ser
416      290      295      300
419 Asp Pro Leu Tyr Thr Pro Glu Pro Asp Thr Cys His Glu Leu Leu Gly
420 305      310      315      320
423 His Val Pro Leu Leu Ala Asp Pro Lys Phe Ala Gln Phe Ser Gln Glu
424      325      330      335
427 Ile Gly Leu Ala Ser Leu Gly Ala Ser Asp Glu Asp Val Gln Lys Leu
428      340      345      350
431 Ala Thr Cys Tyr Phe Phe Thr Ile Glu Phe Gly Leu Cys Lys Gln Glu
432      355      360      365
435 Gly Gln Leu Arg Ala Tyr Gly Ala Gly Leu Leu Ser Ser Ile Gly Glu
436      370      375      380
439 Leu Lys His Ala Leu Ser Asp Lys Ala Cys Val Lys Ser Phe Asp Pro
440 385      390      395      400
443 Lys Thr Thr Cys Leu Gln Glu Cys Leu Ile Thr Thr Phe Gln Asp Ala
444      405      410      415
447 Tyr Phe Val Ser Asp Ser Phe Glu Glu Ala Lys Glu Lys Met Arg Asp
448      420      425      430
451 Phe Ala Lys Ser Ile Thr Arg Pro Phe Ser Val Tyr Phe Asn Arg Tyr
452      435      440      445
455 Thr Gln Ser Ile Glu Ile Leu Lys Asp Thr Arg Ser Ile Glu Asn Val
456      450      455      460
459 Val Gln Asp Leu Arg Ser Asp Leu Asn Thr Val Cys Asp Ala Leu Asn
460 465      470      475      480
463 Lys Met Asn Gln Tyr Leu Gly Ile

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VERIFICATION SUMMARY

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